

Legal

12

PCT09

#9

## RAW SEQUENCE LISTING

PATFNT APPLICATION: US/09/744,847

DATE: 07/27/2001

TIME: 19:42:56

Input Set : A:\IM-3-C1-PCT\_seq.txt

Output Set: N:\CRF3\07272001\I744847.raw

PS

3 <110> APPLICANT: Sim, Gek-Kee  
 4 Dreitz, Matthew J.  
 6 <120> TITLE OF INVENTION: T CELL RECEPTOR PROTEINS, NUCLEIC ACID MOLECULES, AND  
 7 USES THEREOF  
 9 <130> FILE REFERENCE: IM-3-C1-PCT  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/744,847  
 C--> 13 <141> CURRENT FILING DATE: 2001-04-16  
 15 <150> PRIOR APPLICATION NUMBER: 60/094,506  
 16 <151> PRIOR FILING DATE: 1998-07-29  
 18 <160> NUMBER OF SEQ ID NOS: 100  
 20 <170> SOFTWARE: WordPerfect for Windows 8.0  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 381  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Canis familiaris  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (1)..(381)  
 32 <400> SEQUENCE: 1  
 33 atc gga ctc ctc tgt ggt gtg gcc ttt tgt ttc ctg gga gta ggc ctt 48  
 34 ile gly leu leu cys gly val ala phe cys phe leu gly val gly leu  
 35 1 5 10 15  
 37 ttg aac gca caa gtg act caa acc ccg aga caa ctc atc aaa aaa gtg 96  
 38 leu asn ala gln val thr gln thr pro arg gln leu ile lys lys val  
 39 20 25 30  
 41 gga gcg aaa gtt ttg ttg aaa tgt tca cag aat atg gac cat gaa aga 144  
 42 gly ala lys val leu leu lys cys ser gln asn met asp his glu arg  
 43 35 40 45  
 45 atg ttc tgg tat cga caa gac cca ggt ctg ggg ttg cgg ctg ctc tac 192  
 46 met phe trp tyr arg gln asp pro gly leu gly leu arg leu leu tyr  
 47 50 55 60  
 48 tgg tcc tat aat att gac agt gtt gag aca gga gac atc cct tat ggg 240  
 49 trp ser tyr asn ile asp ser val glu thr gly asp ile pro tyr gly  
 50 65 70 75 80  
 52 tac agt gtc tcg agg aag aag aag gat gcc ttc ccc ttg att ctg gag 288  
 53 tyr ser val ser arg lys lys lys asp ala phe pro leu ile leu glu  
 54 85 90 95  
 56 tct gct cgc atc aac cag aca tct gtg tac ttc tgc gcc agc agc ccg 336  
 57 ser ala arg ile asn gln thr ser val tyr phe cys ala ser ser pro  
 58 100 105 110  
 60 ttt agc caa aat acc cag tac ttc ggg gcg ggc acc cgg ctg cta 381  
 61 phe ser gln asn thr gln tyr phe gly ala gly thr arg leu leu  
 62 115 120 125  
 65 <210> SEQ ID NO: 2  
 66 <211> LENGTH: 127  
 67 <212> TYPE: PRT  
 68 <213> ORGANISM: Canis familiaris

ENTERED

## RAW SEQUENCE LISTING

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Input Set : A:\IM-3-C1-PCT\_seq.txt

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70 &lt;400&gt; SEQUENCE: 2

```

71 Ile Gly Leu Leu Cys Gly Val Ala Phe Cys Phe Leu Gly Val Gly Leu
72   1           5           10           15
74 Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val
75           20           25           30
77 Gly Ala Lys Val Leu Leu Lys Cys Ser Gln Asn Met Asp His Glu Arg
78           35           40           45
80 Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu Leu Tyr
81           50           55           60
83 Trp Ser Tyr Asn Ile Asp Ser Val Glu Thr Gly Asp Ile Pro Tyr Gly
84   65           70           75           80
86 Tyr Ser Val Ser Arg Lys Lys Lys Asp Ala Phe Pro Leu Ile Leu Glu
87           85           90           95
89 Ser Ala Arg Ile Asn Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser Pro
90           100          105          110
92 Phe Ser Gln Asn Thr Gln Tyr Phe Gly Ala Gly Thr Arg Leu Leu
93           115          120          125

```

96 &lt;210&gt; SEQ ID NO: 3

97 &lt;211&gt; LENGTH: 381

98 &lt;212&gt; TYPE: DNA

99 &lt;213&gt; ORGANISM: Canis familiaris

101 &lt;400&gt; SEQUENCE: 3

```

102 tagcagccgg gtgcccgccc cgaagtactg ggtatttttg ctaaaccgggc tactggcgca 60
104 gaagtacaca gatgtctggt tgatgcgagc agactccaga atcaagggga aggcatecct 120
106 cttcttcctc gagacactgt acccataagg gatgtctcct gtctcaacac tgtcaatatt 180
108 ataggaccag tagagcagcc gcaaccccag acctgggtct tgatgatacc agaacattct 240
110 ttcatgggtcc atattctgtg aacattttcaa caaaactttc gctcccactt ttttgatgag 300
112 ttgtctcggg gtttgagtca cttgtgcgtt caaaaggcct actcccagga aacaaaaggc 360
114 cacaccacag aggagtccga t                                     381

```

117 &lt;210&gt; SEQ ID NO: 4

118 &lt;211&gt; LENGTH: 408

119 &lt;212&gt; TYPE: DNA

120 &lt;213&gt; ORGANISM: Canis familiaris

122 &lt;220&gt; FEATURE:

123 &lt;221&gt; NAME/KEY: CDS

124 &lt;222&gt; LOCATION: (25)..(408)

126 &lt;400&gt; SEQUENCE: 4

```

127 acggtgaagg gctagcacct aaag atg ctg act tgc ctg cta ctc ctc ctg 51
128           Met Leu Thr Cys Leu Leu Leu Leu
129           1           5
131 gga caa ggc tct gtg ttt gga gct ctt gtc tct caa aag ccg cgc agg 99
132 Gly Gln Gly Ser Val Phe Gly Ala Leu Val Ser Gln Lys Pro Arg Arg
133   10           15           20           25
135 gac atc tgt caa cgt ggg acc tcc att acc atc cac tgt gag gtc gat 147
136 Asp Ile Cys Gln Arg Gly Thr Ser Ile Thr Ile His Cys Glu Val Asp
137           30           35           40
139 acc caa gtc acc ttg atg ttc tgg tac cgt cag ctc cca gga cag agc 195
140 Thr Gln Val Thr Leu Met Phe Trp Tyr Arg Gln Leu Pro Gly Gln Ser
141           45           50           55

```

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Input Set : A:\IM-3-C1-PCT\_seq.txt

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```

143 ttg ata ctg att gca acc gca aac cag ggt gca gag gcc acc tac gaa 243
144 Leu Ile Leu Ile Ala Thr Ala Asn Gln Gly Ala Glu Ala Thr Tyr Glu
145      60      65      70
147 agt gga ttt acc agg gag aag ttt ccc atc agc cgc cga acc cta atg 291
148 Ser Gly Phe Thr Arg Glu Lys Phe Pro Ile Ser Arg Arg Thr Leu Met
149      75      80      85
151 ttc tcc act ctg act gtg agc aac ctg agc ctc gaa gac acc agc tct 339
152 Phe Ser Thr Leu Thr Val Ser Asn Leu Ser Leu Glu Asp Thr Ser Ser
153 90      95      100      105
155 tac ttc tgc agc att tgg tac ggg gag ggg gag cag cac ttt ggg cca 387
156 Tyr Phe Cys Ser Ile Trp Tyr Gly Glu Gly Glu Gln His Phe Gly Pro
157      110      115      120
159 ggg acc cgg ctc acc gtc cta 408
160 Gly Thr Arg Leu Thr Val Leu
161      125
164 <210> SEQ ID NO: 5
165 <211> LENGTH: 128
166 <212> TYPE: PRT
167 <213> ORGANISM: Canis familiaris
169 <400> SEQUENCE: 5
170 Met Leu Thr Cys Leu Leu Leu Leu Leu Gly Gln Gly Ser Val Phe Gly
171 1      5      10      15
173 Ala Leu Val Ser Gln Lys Pro Arg Arg Asp Ile Cys Gln Arg Gly Thr
174      20      25      30
176 Ser Ile Thr Ile His Cys Glu Val Asp Thr Gln Val Thr Leu Met Phe
177      35      40      45
179 Trp Tyr Arg Gln Leu Pro Gly Gln Ser Leu Ile Leu Ile Ala Thr Ala
180      50      55      60
182 Asn Gln Gly Ala Glu Ala Thr Tyr Glu Ser Gly Phe Thr Arg Glu Lys
183 65      70      75      80
185 Phe Pro Ile Ser Arg Arg Thr Leu Met Phe Ser Thr Leu Thr Val Ser
186      85      90      95
187 Asn Leu Ser Leu Glu Asp Thr Ser Ser Tyr Phe Cys Ser Ile Trp Tyr
188      100      105      110
190 Gly Glu Gly Glu Gln His Phe Gly Pro Gly Thr Arg Leu Thr Val Leu
191      115      120      125
194 <210> SEQ ID NO: 6
195 <211> LENGTH: 408
196 <212> TYPE: DNA
197 <213> ORGANISM: Canis familiaris
199 <400> SEQUENCE: 6
200 taggacggtg agccgggtcc ctggcccaaa gtgctgctcc cctccccgt accaaatgct 60
202 gcagaagtaa gagctggtgt ctgcaggct caggttgctc acagtcagag tggagaacat 120
204 taggggtcgg cggctgatgg gaaacttctc cctggtaaata ccactttcgt aggtggcctc 180
206 tgcaccctgg tttgcggttg caatcagtat caagctctgt cctgggagct gacggtacca 240
208 gaacatcaag gtgacttggg tatcgacctc acagtggatg gtaatggagg tcccacgttg 300
210 acagatgtcc ctgcgcggct tttgagagac aagagctcca aacacagagc cttgtcccag 360
212 gaggagtagc aggcaagtca gcattcttag gtgctagccc ttcaccgt 408
215 <210> SEQ ID NO: 7

```

## RAW SEQUENCE LISTING

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Input Set : A:\IM-3-C1-PCT\_seq.txt

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```

216 <211> LENGTH: 384
217 <212> TYPE: DNA
218 <213> ORGANISM: Canis familiaris
220 <400> SEQUENCE: 7
221 atg ctg act tgc ctg cta ctc ctc ctg gga caa ggc tct gtg ttt gga      48
222 Met Leu Thr Cys Leu Leu Leu Leu Leu Gly Gln Gly Ser Val Phe Gly
223   1           5           10           15
225 gct ctt gtc tct caa aag ccg cgc agg gac atc tgt caa cgt ggg acc      96
226 Ala Leu Val Ser Gln Lys Pro Arg Arg Asp Ile Cys Gln Arg Gly Thr
227           20           25           30
229 tcc att acc atc cac tgt gag gtc gat acc caa gtc acc ttg atg ttc      144
230 Ser Ile Thr Ile His Cys Glu Val Asp Thr Gln Val Thr Leu Met Phe
231           35           40           45
233 tgg tac cgt cag ctc cca gga cag agc ttg ata ctg att gca acc gca      192
234 Trp Tyr Arg Gln Leu Pro Gly Gln Ser Leu Ile Leu Ile Ala Thr Ala
235           50           55           60
237 aac cag ggt gca gag gcc acc tac gaa agt gga ttt acc agg gag aag      240
238 Asn Gln Gly Ala Glu Ala Thr Tyr Glu Ser Gly Phe Thr Arg Glu Lys
239           65           70           75           80
241 ttt ccc atc agc cgc cga acc cta atg ttc tcc act ctg act gtg agc      288
242 Phe Pro Ile Ser Arg Arg Thr Leu Met Phe Ser Thr Leu Thr Val Ser
243           85           90           95
245 aac ctg agc ctc gaa gac acc agc tct tac ttc tgc agc att tgg tac      336
246 Asn Leu Ser Leu Glu Asp Thr Ser Ser Tyr Phe Cys Ser Ile Trp Tyr
247           100          105          110
248 ggg gag ggg gag cag cac ttt ggg cca ggg acc cgg ctc acc gtc cta      384
249 Gly Glu Gly Glu Gln His Phe Gly Pro Gly Thr Arg Leu Thr Val Leu
250           115          120          125
253 <210> SEQ ID NO: 8
254 <211> LENGTH: 384
255 <212> TYPE: DNA
256 <213> ORGANISM: Canis familiaris
W--> 257 <400> SEQUENCE: 8
258 taggacggtg agcgggtcc ctggcccaaa gtgctgctcc ccctcccgt accaaatgct 60
260 gcagaagtaa gagctggtgt ctgcaggct caggttgctc acagtcagag tggagaacat 120
262 tagggttcgg cggctgatgg gaaacttctc cctggtaa atccactttcgt aggtggcctc 180
264 tgcaccctgg tttgcggttg caatcagtat caagctctgt cctgggagct gacggtacca 240
266 gaacatcaag gtgacttggg tatcgacctc acagtggatg gtaatggagg tcccacgttg 300
268 acagatgtcc ctgcgcggct tttgagagac aagagctcca aacacagagc cttgtcccag 360
270 gaggagtagc aggcaagtca gcat                                     384
273 <210> SEQ ID NO: 9
274 <211> LENGTH: 408
275 <212> TYPE: DNA
276 <213> ORGANISM: Canis familiaris
278 <220> FEATURE:
279 <221> NAME/KEY: CDS
280 <222> LOCATION: (7)..(408)
282 <400> SEQUENCE: 9
283 gctgaa atg gcc acc ggc gtc ttc ttt ggc atg gct ctt tgt gtc ctg      48

```

## RAW SEQUENCE LISTING

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Input Set : A:\IM-3-C1-PCT\_seq.txt

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```

284      Met Ala Thr Gly Val Phe Phe Gly Met Ala Leu Cys Val Leu
285          1          5          10
287 tgg aca gga tac atg gat gct gga att atc cag agc cca aga tac aag      96
288 Trp Thr Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys
289 15          20          25          30
291 gtc aca ggg aca gga aag agg gtg act ctg aga tgt cac cag aca gac      144
292 Val Thr Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp
293          35          40          45
295 aac tat gac tat atg tac tgg tat cga cat gac ctg gga cat ggg ccg      192
296 Asn Tyr Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro
297          50          55          60
299 agg ctg atc tat tat tca aat ggt att aac agc act gaa aaa gga gac      240
300 Arg Leu Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp
301          65          70          75
303 ctc tcc aat gga tac aca gtc tct aga tca aac aag atg gat ttc ccc      288
304 Leu Ser Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro
305      80          85          90
307 ctc cta ctg gac tct gtt acc tcc tcc cag aca tct gtg tac ttc tgt      336
308 Leu Leu Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys
309 95          100          105          110
311 gcc gac acg agg gat cct gtt gca gta aat tat gat ttt aac ttt ggc      384
312 Ala Asp Thr Arg Asp Pro Val Ala Val Asn Tyr Asp Phe Asn Phe Gly
313          115          120          125
315 cca ggg acc aag ctg aca gtc gta      408
316 Pro Gly Thr Lys Leu Thr Val Val
317      130
320 <210> SEQ ID NO: 10
321 <211> LENGTH: 134
322 <212> TYPE: PRT
323 <213> ORGANISM: Canis familiaris
325 <400> SEQUENCE: 10
326 Met Ala Thr Gly Val Phe Phe Gly Met Ala Leu Cys Val Leu Trp Thr
327 1          5          10          15
329 Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys Val Thr
330          20          25          30
332 Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp Asn Tyr
333          35          40          45
335 Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro Arg Leu
336          50          55          60
338 Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp Leu Ser
339 65          70          75          80
341 Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro Leu Leu
342          85          90          95
344 Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys Ala Asp
345          100          105          110
347 Thr Arg Asp Pro Val Ala Val Asn Tyr Asp Phe Asn Phe Gly Pro Gly
348          115          120          125
350 Thr Lys Leu Thr Val Val
351      130

```



Use of a codon for Val has been detected in the Sequence Listing.  
 Review the listing and determine if the use of the codon for Val is  
 correct. If not, please correct the listing to reflect the correct use of  
 the codon for Val.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/744,847

DATE: 07/27/2001

TIME: 19:42:57

Input Set : A:\IM-3-C1-PCT\_seq.txt

Output Set : N:\CRF3\07272001\I744847.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:257 M:283 W: Missing Blank Line separator, <400> field identifier  
L:732 M:283 W: Missing Blank Line separator, <220> field identifier  
L:974 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1521 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1660 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1748 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:60  
L:1748 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:60  
L:1748 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60  
L:1780 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:61  
L:1780 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:61  
L:1780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61  
L:1811 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:62  
L:1811 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:62  
L:1811 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62  
L:1841 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:63  
L:1841 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:63  
L:1841 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63  
L:1872 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:64  
L:1872 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:64  
L:1872 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64  
L:1902 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:65  
L:1902 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:65  
L:1902 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65  
L:1933 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:66  
L:1933 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:66  
L:1933 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66  
L:1963 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:67  
L:1963 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:67  
L:1963 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67  
L:1994 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:68  
L:1994 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:68  
L:1994 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68  
L:1997 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:68  
L:1997 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:68  
L:1997 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68  
L:2028 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:69  
L:2028 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:69  
L:2028 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69  
L:2059 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:70  
L:2059 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:70  
L:2059 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70  
L:2070 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2089 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:71  
L:2089 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:71  
L:2089 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71  
L:2092 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:71

## VERIFICATION SUMMARY

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Input Set : A:\IM-3-C1-PCT\_seq.txt

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L:2092 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:71  
L:2092 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71  
L:2122 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:72  
L:2122 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:72  
L:2122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72  
L:2153 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:73  
L:2153 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:73  
L:2153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73  
L:2184 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:74  
L:2184 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:74  
L:2184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74  
L:2192 M:283 W: Missing Blank Line separator, <220> field identifier  
L:2214 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:75  
L:2214 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:75  
L:2214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75  
L:2245 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:76  
L:2245 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:76  
L:2245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76  
L:2248 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:76  
L:2248 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:76  
L:2248 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76  
L:2278 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:77  
L:2278 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:77  
L:2278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77  
L:2281 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:77  
L:2281 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:77  
L:2281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77  
L:2311 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:78  
L:2311 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:78  
L:2311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78  
L:2343 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:79  
L:2343 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:79  
L:2343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79  
L:2374 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:80  
L:2374 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:80  
L:2374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80  
L:2389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81